

F. Young

PCT04

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/762,194

DATE: 05/29/2001

TIME: 15:53:16

Input Set : A:\Seqlist.txt

Output Set: C:\CRF3\05292001\I762194.raw

ENTERED

4 <110> APPLICANT: Elbaz, Nathalie
 5 Nahmias, Clara
 6 Strosberg, Arthur Donny
 8 <120> TITLE OF INVENTION: NUCLEIC SEQUENCES ENCODING AN AT2
 9 RECEPTOR-INTERACTING PROTEIN (ATIP) AND THEIR APPLICATIONS
 13 <130> FILE REFERENCE: 33339/208804
 15 <140> CURRENT APPLICATION NUMBER: US 09/762,194
 C--> 16 <141> CURRENT FILING DATE: 2001-04-19
 18 <150> PRIOR APPLICATION NUMBER: PCT/FR99/01908
 19 <151> PRIOR FILING DATE: 1999-08-02
 21 <150> PRIOR APPLICATION NUMBER: FR 98/09997
 22 <151> PRIOR FILING DATE: 1998-08-04
 24 <160> NUMBER OF SEQ ID NOS: 12
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 1803
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Mus musculus
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (178)...(1500)
 37 <400> SEQUENCE: 1
 38 gctaccccc cccacgcac cccccaatct ggggtggcctg gcattagcat gtaagcttgt 60
 39 tttctctgg ctgtatctct tggcctggaa gaaccccgag ttgccaaag acacagtatg 120
 40 tgatggtccc tggaaaaact gcttcccctg cgaagtcttc ccactggctt cgaagac atg 180
 41 Met
 42 1
 44 ctg ttg tct ecc aaa ttc tcc tta tcc acc atc cac gtc cgc cta acc 228
 45 Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu Thr
 46 5 10 15
 48 gcc aaa gga ctg ctt cga aac ctg cgg ctt cct tcg ggg ctg agg aaa 276
 49 Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg Lys
 50 20 25 30
 52 aac act gtc att ttc cac aca gtt gaa aag ggc agg cag aag aat ccc 324
 53 Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn Pro
 54 35 40 45
 56 agg agc ctg tgc atc cag acc cag aca gct cca gat gtg ctg tcc tcc 372
 57 Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser Ser
 58 50 55 60 65
 60 gag aga acg ctt gag ttg gcc caa tac aag aca aaa tgt gaa agc caa 420
 61 Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser Gln
 62 70 75 80
 64 agt gga ttc atc ctg cac ctg agg cag ctt ctt tcc cgt ggt aac aac 468
 65 Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn Asn
 66 85 90 95
 68 aag ttt gaa gcg ctg aca gtt gtg atc cag cac ctg ctg tct gag cgg 516
 69 Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu Arg

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70	100	105	110	
72	gag gaa gca ctg aag caa cac aaa acc ctc tct caa gaa ctt gtc agc	564		
73	Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val Ser			
74	115	120	125	
76	ctc cgg gga gag cta gtt gct gct tca agc gcc tgt gag aag cta gaa	612		
77	Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu Glu			
78	130	135	140	145
80	aag gct agg gct gac tta cag aca gcg tat caa gaa ttt gtc cag aaa	660		
81	Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln Lys			
82	150	155	160	
84	cta aac cag cag cat cag aca gac cgg acg gaa ctg gag aac cgg ctg	708		
85	Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu			
86	165	170	175	
88	aag gac tta tac acc gca gag tgt gag aag ctt cag agc att tac att	756		
89	Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile			
90	180	185	190	
92	gag gag gca gaa aaa tat aaa act caa ctg caa gag cag ttt gac aac	804		
93	Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn			
94	195	200	205	
96	tta aac gcc gcc cat gag acc act aag ctt gag att gaa gct agc cac	852		
97	Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His			
98	210	215	220	225
100	tcg gag aag gtg gaa ttg ctg aag aag acc tat gaa acc tcc ctt tca	900		
101	Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser			
102	230	235	240	
104	gaa atc aag aag agc cat gag atg gag aag aag tca ctg gag gat ctg	948		
105	Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu			
106	245	250	255	
108	ctt aat gag aag cag gaa tcg ctg gag aaa caa atc aat gat ctg aag	996		
109	Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys			
110	260	265	270	
112	agt gaa aac gat gct tta aac gaa agg ttg aaa tca gag gag caa aag	1044		
113	Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln Lys			
114	275	280	285	
116	caa ctg tca aga gag aag gcg aat tcc aaa aac cct cag gtc atg tat	1092		
117	Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met Tyr			
118	290	295	300	305
120	ctg gag caa gaa cta gaa agc ctg aag gct gtg tta gag atc aag aat	1140		
121	Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn			
122	310	315	320	
124	gag aag ctg cac cag cag gac atg aag cta atg aag atg gaa aag ctg	1188		
125	Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys Leu			
126	325	330	335	
128	gtg gac aat aac aca gca ttg gtt gac aag ctg aag cga ttc cag cag	1236		
129	Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln			
130	340	345	350	
132	gaa aac gag gag tta aaa gct cgc atg gac aaa cac atg gca att tca	1284		
133	Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile Ser			
134	355	360	365	

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136 agg caa ctt tcc acc gag cag gcc gcg ctg caa gag tcc ctt gag aag      1332
137 Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu Lys
138 370                               375                               380                               385
140 gag tca aag gtc aac aag aga ctg tcc atg gag aac gag gaa ctt ctg      1380
141 Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu Leu
142                               390                               395                               400
144 tgg aaa ctg cac aac gga gac ctg tgc agc ccc aag aga tcc ccc acc      1428
145 Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro Thr
146                               405                               410                               415
148 tcc tcg gcc atc cct ttc cag tcc ccc agg aat tct ggt tcc ttc tcc      1476
149 Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe Ser
150                               420                               425                               430
152 agc ccc agc atc tca ccc aga tga/cggcttctga acgcaggaga ctctctgaag      1530
153 Ser Pro Ser Ile Ser Pro Arg *
154                               435                               440
156 gcactgaggt gcgcttctgc aggaactgacc ctctcatggg aactcgagtt gctgcggttag      1590
157 ctctctggaa tatccccagg atatcgggag agcagccgcc aaccgtatca gctacgtacg      1650
158 aatagagagc tccaatagaa gacttttaac ttggtccaaa agcctcctcc aaaaacagat      1710
159 ttcggaactg aagtggacat agttgcacaa agcacttacg gaacgaggga acctgtttct      1770
160 ttgcttctct tcaactaagc ataggctttc cag                                1803
162 <210> SEQ ID NO: 2
163 <211> LENGTH: 440
164 <212> TYPE: PRT
165 <213> ORGANISM: Mus musculus
167 <400> SEQUENCE: 2
168 Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu
169 1 5 10 15
170 Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg
171 20 25 30
172 Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn
173 35 40 45
174 Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser
175 50 55 60
176 Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser
177 65 70 75 80
178 Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn
179 85 90 95
180 Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu
181 100 105 110
182 Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val
183 115 120 125
184 Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu
185 130 135 140
186 Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln
187 145 150 155 160
188 Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
189 165 170 175
190 Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
191 180 185 190

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192 Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp
193      195      200      205
194 Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
195      210      215      220
196 His Ser Glu Lys Val Glu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
197 225      230      235      240
198 Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
199      245      250      255
200 Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
201      260      265      270
202 Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
203      275      280      285
204 Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
205      290      295      300
206 Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys
207 305      310      315      320
208 Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys
209      325      330      335
210 Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln
211      340      345      350
212 Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile
213      355      360      365
214 Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu
215      370      375      380
216 Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu
217 385      390      395      400
218 Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro
219      405      410      415
220 Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe
221      420      425      430
222 Ser Ser Pro Ser Ile Ser Pro Arg
223      435      440
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 1323
227 <212> TYPE: DNA
228 <213> ORGANISM: Mus musculus
230 <220> FEATURE:
231 <221> NAME/KEY: CDS
232 <222> LOCATION: (1)...(1323)
234 <400> SEQUENCE: 3
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236 Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu
237 1      5      10      15
239 acc gcc aaa gga ctg ctt cga aac ctc cgg ctt cct tcg ggg ctc agg      96
240 Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg
241      20      25      30
243 aaa aac act gtc att ttc cac aca gtt gaa aag ggc agg cag aag aat      144
244 Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn
245      35      40      45

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247	ccc	agg	agc	ctg	tgc	atc	cag	acc	cag	aca	gct	cca	gat	gtg	ctg	tcc	192
248	Pro	Arg	Ser	Leu	Cys	Ile	Gln	Thr	Gln	Thr	Ala	Pro	Asp	Val	Leu	Ser	
249	50					55					60						
251	tcc	gag	aga	acg	ctt	gag	ttg	gcc	caa	tac	aag	aca	aaa	tgt	gaa	agc	240
252	Ser	Glu	Arg	Thr	Leu	Glu	Leu	Ala	Gln	Tyr	Lys	Thr	Lys	Cys	Glu	Ser	
253	65					70					75					80	
255	caa	agt	gga	ttc	atc	ctg	cac	ctc	agg	cag	ctt	ctt	tcc	cgt	ggt	aac	288
256	Gln	Ser	Gly	Phe	Ile	Leu	His	Leu	Arg	Gln	Leu	Leu	Ser	Arg	Gly	Asn	
257	85					85					90					95	
259	aac	aag	ttt	gaa	gcg	ctg	aca	ggt	gtg	atc	cag	cac	ctc	ctg	tct	gag	336
260	Asn	Lys	Phe	Glu	Ala	Leu	Thr	Val	Val	Ile	Gln	His	Leu	Leu	Ser	Glu	
261	100					100					105					110	
263	cgg	gag	gaa	gca	ctg	aag	caa	cac	aaa	acc	ctc	tct	caa	gaa	ctt	gtc	384
264	Arg	Glu	Glu	Ala	Leu	Lys	Gln	His	Lys	Thr	Leu	Ser	Gln	Glu	Leu	Val	
265	115					120										125	
267	agc	ctc	cgg	gga	gag	cta	ggt	gct	gct	tca	agc	gcc	tgt	gag	aag	cta	432
268	Ser	Leu	Arg	Gly	Glu	Leu	Val	Ala	Ala	Ser	Ser	Ala	Cys	Glu	Lys	Leu	
269	130					135						140					
271	gaa	aag	gct	agg	gct	gac	tta	cag	aca	gcg	tat	caa	gaa	ttt	gtc	cag	480
272	Glu	Lys	Ala	Arg	Ala	Asp	Leu	Gln	Thr	Ala	Tyr	Gln	Glu	Phe	Val	Gln	
273	145					150					155					160	
275	aaa	cta	aac	cag	cag	cat	cag	aca	gac	cgg	acg	gaa	ctg	gag	aac	cgg	528
276	Lys	Leu	Asn	Gln	Gln	His	Gln	Thr	Asp	Arg	Thr	Glu	Leu	Glu	Asn	Arg	
277	165					165					170					175	
279	ctg	aag	gac	tta	tac	acc	gca	gag	tgt	gag	aag	ctt	cag	agc	att	tac	576
280	Leu	Lys	Asp	Leu	Tyr	Thr	Ala	Glu	Cys	Glu	Lys	Leu	Gln	Ser	Ile	Tyr	
281	180					185										190	
283	att	gag	gag	gca	gaa	aaa	tat	aaa	act	caa	ctg	caa	gag	cag	ttt	gac	624
284	Ile	Glu	Glu	Ala	Glu	Lys	Tyr	Lys	Thr	Gln	Leu	Gln	Glu	Gln	Phe	Asp	
285	195					200										205	
287	aac	tta	aac	gcc	gcc	cat	gag	acc	act	aag	ctt	gag	att	gaa	gct	agc	672
288	Asn	Leu	Asn	Ala	Ala	His	Glu	Thr	Thr	Lys	Leu	Glu	Ile	Glu	Ala	Ser	
289	210					215										220	
291	cac	tcg	gag	aag	gtg	gaa	ttg	ctg	aag	aag	acc	tat	gaa	acc	tcc	ctt	720
292	His	Ser	Glu	Lys	Val	Glu	Leu	Leu	Lys	Lys	Thr	Tyr	Glu	Thr	Ser	Leu	
293	225					230										235	
295	tca	gaa	atc	aag	aag	agc	cat	gag	atg	gag	aag	aag	tca	ctg	gag	gat	768
296	Ser	Glu	Ile	Lys	Lys	Ser	His	Glu	Met	Glu	Lys	Lys	Ser	Leu	Glu	Asp	
297	245					250										255	
299	ctg	ctt	aat	gag	aag	cag	gaa	tcg	ctg	gag	aaa	caa	atc	aat	gat	ctg	816
300	Leu	Leu	Asn	Glu	Lys	Gln	Glu	Ser	Leu	Glu	Lys	Gln	Ile	Asn	Asp	Leu	
301	260					265										270	
303	aag	agt	gaa	aac	gat	gct	tta	aac	gaa	agg	ttg	aaa	tca	gag	gag	caa	864
304	Lys	Ser	Glu	Asn	Asp	Ala	Leu	Asn	Glu	Arg	Leu	Lys	Ser	Glu	Glu	Gln	
305	275					280										285	
307	aag	caa	ctg	tca	aga	gag	aag	gcg	aat	tcc	aaa	aac	cct	cag	gtc	atg	912
308	Lys	Gln	Leu	Ser	Arg	Glu	Lys	Ala	Asn	Ser	Lys	Asn	Pro	Gln	Val	Met	
309	290					295										300	
311	tat	ctg	gag	caa	gaa	cta	gaa	agc	ctg	aag	gct	gtg	tta	gag	atc	aag	960

VERIFICATION SUMMARY

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date